

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 26, 2002, 20:33:06 ; Search time 1934 Seconds

(without alignments)
4836.293 Million cell updates/sec

Title: US-09-840-795-18_COPY_78_770

Perfect score: 693

Sequence: 1 atggatttgcacaaatga.....agcagcaggccatgt 693

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 2747214

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_estbun:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_lestro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_gss:*

13: em_gss_hum:*

14: em_gss_inv:*

15: em_gss_pln:*

16: em_gss_vrt:*

SUMMARIES

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

Score Query Length DB ID Description

RESULT 1 BB219800 BB219800

LOCUS BB219800 RIKEN full-length enriched mRNA linear EST 23-oct-2001

DEFINITION mmusculus cDNA clone A530057A22 3', mRNA sequence.

ACCESSION BB219800

VERSION BB219800.2 GI:16353450

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

MATERIAL: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 689)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Samo,H., Sasaki,D., Shibata,K., Shinagawa,A., Shikai,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.

TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

JOURNAL Unpublished (2001)

COMMENT On Jun 30, 2000 this sequence version replaced gi:8884753.

Contact: Yoshihiko Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

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Email: genome-rss@gsc.riken.go.jp;

URL: http://genome.gsc.riken.go.jp/

Carnici,P., Shibata,Y., Hayashizaki,Y., Sugihara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected DNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)

wagi,K., Fujiwara,S., Inoue,K., Toda,Y., Izawa,M., Ohara,E., wataki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunaga,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and

18	76.6	11.1	-	401	9	AA003356
19	71.8	10.4	-	526	9	BB856841
20	67.9	9.7	-	358	9	AA03247
21	64.4	9.3	-	499	9	BB85206
22	60.2	8.7	-	678	9	BB641271
23	59.6	8.6	-	673	10	BI94967
24	58.2	8.4	-	1110	12	CNS50TC
25	57	8.2	-	626	9	BB652914
26	52.4	7.6	-	275	9	AV11112
27	47.6	6.9	-	282	9	AL030000
28	42.4	6.6	-	612	12	AQ031525
29	42.2	6.1	-	670	10	BI23347
30	39.6	5.7	-	708	9	AL653137
31	39.2	5.7	-	803	9	AL563968
32	38.6	5.6	-	547	10	BG87869
33	38.6	5.6	-	568	10	BM010615
34	38.6	5.6	-	641	10	BE226747
C	35	38.6	-	705	9	AL580892
36	38.6	5.6	-	713	10	BG72816
37	38.6	5.6	-	817	10	BG575868
38	38.6	5.6	-	884	10	BG66700
39	38.6	5.6	-	889	10	BI52640
40	38.6	5.6	-	939	10	BI520358
41	38.6	5.6	-	970	9	AL551177
42	38.6	5.6	-	1048	10	BM448980
43	38.6	5.6	-	1067	10	BF037815
44	38.6	5.6	-	1095	10	BG391978
45	38.6	5.6	-	1176	10	BI911227

ALIGNMENTS

AA003356	mg49g01.r
BB856841	BB856841
AA03247	ml74a03.r
BB85206	BB85206
BB641271	BB641271
BI94967	BI94967
AL47097	Tetraodon
BB652914	BB652914
AV11112	AV11112
AL030000	DKF05564K
AG021525	CIT-HSP-2
BL253347	603973621
AL653137	AL653137
AL669968	AL563968
BG87869	H01-1AA
BM010615	BM010615
BE226747	601178305
AL580892	AL580892
BG52816	602132651
BS75868	602598686
BG66700	60265716
BI52640	603175660
BI520358	603071833
AL551177	AL551177
BM448980	AGENCOURT
BF037815	601461984
BG391978	602409928
BI911227	603062988

Db	60	TGGATTCGCAAGAAATGAGTACTTGGGACAACTTGGGACGGGTGTACCTTCACCA
Qy	56	AACGGTGCTGCTCGTGACAGGAGCTATCCAGGATCTGTTATGGAGA-GGGTGGAGAT
Db	115	GCTTACTGCACGCCCTCGCAGGACAAAGAACAGCTGGGCCACACAAATG
Db	115	GCTTACTGCACGCCCTCGCAGGACAAAGAACAGCTGGGCCACACAAATG
Qy	175	CAGAGTTGCATCACCTGTGTCATCAATCGTGTACAGGAGTCACTCACAG-CTAC
Db	240	CAGAGTTGCATCACCTGTGTCATCAATCGTGTACAGGAGTCACTCACAG-CTAC
Db	240	CAGAGTTGCATCACCTGTGTCATCAATCGTGTACAGGAGTCACTCACAG-CTAC
Qy	294	CCTGGAGGAC-AAGAGTGAATCCGGCAGGAAGAGACCCACCTCTGAGGTCAAT
Db	350	CTTCAGGACCAAAGAGTGCATCCCGTGCAGGAAGCAGACAGCATGGAGG
Qy	353	GTGCGCTTCAGTGA-GCTTAGTGA -GGAGATGACCCACAGTGCCTCAGAGG
Db	420	GTGCGCTTCAGTGA -GGAGATGACCCACAGTGCCTCAGAGG
Qy	411	CACACTTGACTGGTG-GCACGCCTGC-TAGTGTTACCTCTGGCTCTGGG
Db	480	CACACTTGACTGGTG-GCACGCCTGC-TAGTGTTACCTCTGGCTCTGGG
Qy	469	CACACTTGACTGGTG-GCACGCCTGC-TAGTGTTACCTCTGGCTCTGGG
Db	540	ATCTCTCTCTACTGCAGCAGTCTAACAGACTATGGCCAAGCGTGGG
Qy	525	GCTGCAAGTGTAGGCTG-ATAAAACAGCAAGGGAATCTCT
Db	600	GCTGCAAGTGTAGGCTG-ATAAAACAGCAAGGGAATCTCT
RESULT 3		
LOCUS	BB627119	BB627119 RIKEN full-length enriched, 12 days embryo, embryonic body
DEFINITION		between diaphragm region and neck Mus musculus cDNA clone
ACCESSION	BB627119	9430060m22 5', mRNA sequence.
VERSION	BB627119.1	GI:16464896
KEYWORDS	EST.	house mouse.
SOURCE	Mus musculus	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurogathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 697)	
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,I., Okido,T., Saito,R., Sakai,C., Sakai,K., Sanoh,H., Sasaki,D., Shibata,K., Shingora,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.	
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)	
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp/ URL: http://genome-gsc.riken.go.jp/ Carninci,P., Shibata,K., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh	
FEATURES	source	
BASE COUNT	184	a 166 c 172 g 175 t
ORIGIN		
Query	1	ATGGATTGCCAAGAAANGAGTACTGGGACCAATGGGACGGTGTACCTGCCACGG
Match	1	ATGGATTGCCAAGAAANGAGTACTGGGACCAATGGGACGGTGTACCTGCCACGG
Best Local Similarity	51.8%	Score 359.2; DB 9; Length 697;
Matches	422;	Conservative 85.8%; Pred. No. 4.7e-91;
		0; Mismatches 68; Indels 2; Gaps 2;
		Matches 422; Conservative 85.8%; Pred. No. 4.7e-91;
		0; Mismatches 68; Indels 2; Gaps 2;
Qy	1	ATGGATTGCCAAGAAANGAGTACTGGGACCAATGGGACGGTGTACCTGCCACGG
Db	182	ATGGATTGCCAAGAAANGAGTACTGGGACCAATGGGACGGTGTACCTGCCACGG
Qy	61	TGCGTCTGGACAGGACATCCAGGATGTTATGGGACGGTGTACCTGCCACGG
Db	242	TGCGCCTGGACAGGACATCCAGGATGTTATGGGACGGTGTACCTGCCACGG
Qy	121	TGCACGCCCTCTGGCAGGTACAAGAGACTGGGGCCACACAAATGAGT
Db	302	TGCATAGCTGCCCTCCGAAGATTAAGACTTGGGACATCACAGATGTCAGCA
Qy	181	TGCATACCTGCTGTCATCAATGGTGTACAGTCACACTCTAAT
Db	362	TGCATACCTGCTGTCATCAATGGGCCAGAGGCCACTCCACAAATCTCAAT

VERSION	BB637179.1
KEYWORDS	EST; house mouse.
SOURCE	Mus musculus
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
REFERENCE	1 (bases 1 to 614)
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Mizazaki,A., Nomura,K., Ono,M., Sakai,C., Sakai,K., Samo,H., Sasaki,H., Tagami,M., Tagava,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE	Unpublished (2001)
JOURNAL	RIKEN Mouse ESTS (T., et al. 2001)
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp/ URL: http://genome.gsc.riken.go.jp/
BASE COUNT	166 a 145 c 156 g 147 t
ORIGIN	
Query Match	42.0%; Score 291; DB 9; Length 614;
Best Local Similarity	85.9%; Pred. No. 9.9e-72;
Matches	346; Conservative 0; Mismatches 55; Indels 2; Gaps 2;
QY	1 ATGGATTCTCAAGAATCAGTAGCTGAGGACAACTGGGACCAATGGGACGGTGTGACCTGCCAACCG 60
Db	182 ATGGATTCTCAAGAATCAGTAGCTGAGGACAACTGGGACGGTGTGACCTGCCAACAA 241
QY	61 TGTGTTCCCTGGAGAGGACTATCCAAGATTGCGTTTGAGAGGGGAGATGCCAC 120
Db	242 TGTGTTCCCTGGAGAGGACTATCCAAGATTGCGTTTGAGAGGGGAGATGCCAC 301
QY	121 TGCACAGCTGCCCTCCGCCAGGTACAGAAGGACTGGCCACCAATGTCAGGT 180
Db	302 TGCATAGTCAGCTGCCCTCCGCCAGGTACAGAAGGACTGGGACATCACAGATCAGACA 361
QY	181 TGATCACCTGTGCTGTCATACTGTTCTCAGAAGGTCACCTGCACAGCTACCTCTAT 240
Db	352 TGCATCACTGTGCTGTCATCATCGGGTCAGAAGGGCAACTGCACAAATCCTCTAT 421
QY	241 GCTGTCTCTGGGACTGTGTGCCAGGTCTACCGAAGACGATGCCATGGAGGCCCTCGAG 300
Db	422 GCTATCTCTGGAGACTGTGTGCCAGGTCTACCGAAGACGATGCCATGGAGGCCCTCGAG 481
QY	301 GACCAAGATGTCATCCCAGCAGAGGACCCCCACCTCTGAGGTCAATGTGCC-TT 359
Db	482 GACCAAGATGTCATCCCAGTACAAGCAGACTCTTCGGAGGTATGGTACCTTT 541
QY	360 CCAGTTGAGCTTGTGGAGGTTAGTGGTACACTGGTCCCC 401
Db	542 CCAGTTGAGCTTGTGGAGGTTAGTGGTACACTGGTCCCC 584
RESULT	6
BB858916	
LOCUS	BB858916
DEFINITION	BB858916 RIKEN full-length enriched, kidney CCL-142 RAG CDNA MUS
MUSCULUS	
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)	
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.	
e mouse tissues.	
FEATURES	
source	
1. -614	
/organism="Mus musculus"	
/ab_xref="taxon:1009"	
/clone="A53005TA22"	
/clone_1ib="RIKEN full-length enriched, adult male aorta and vein"	
/sex="male"	
/tissue_type="aorta and vein"	
/dev_stage="adult"	
/lab_host="DHIOB"	
/note="Site_1: Sali; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'-GAGAGAGAGAGGTCAGAGCTCTTTTTTTVN 3'], cDNA was prepared by using therholose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second	
REFERENCE	1 (bases 1 to 459)
AUTHORS	Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayashi,N., Hiramoto,K., Hirooka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shiba,K., Shinagawa,A., Shiraki,T., Sugabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku,Akamira,S., Tanaka,T., Tomaru,A., Toya,T., Watanuki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE	2001)
JOURNAL	Unpublished (2001)
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp,

strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGCTCGAGTAAATCCATCCCCCCCC 3']. cDNA was cleaved with XbaI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

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URL:<http://genome.gsc.riken.go.jp/>
 Carninci, P., Shihata, Y., Hayashi, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)
 Nagai, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

FEATURES source

Location/Qualifiers

1. .459

/organism="Mus musculus"

/db_xref="taxon:0090"

/clone_id="G43003D23"

/clone_lib="RIKEN full-length enriched, kidney CCL-142 RAG cDNA"

/tissue_type="kidney"

/cell_line="CCL-142 RAG"

BASE COUNT

136 a

98 c

116 g

109 t

ORIGIN

1

Query Match

27.0%

Score 186.8;

DB 9;

Length 459;

Best Local Similarity

86.6%

Pred. No. 3.2e-42;

Matches 206;

Conservative

0;

Mismatches 32;

Indels 0;

Gaps 0;

Qy 1 ATGGATTGCCAAGAAATGAGTACTGGGACCAATGGGAGCGTGTGACTGCCAACGG

Db 222 ATGGATTGTCAGAGAATGAGTACTGGGACCAATGGGGCGCTGTGTCACCTGCCAACAA

Qy 61 TGTGCTCTGGACAGGAGCTATCCAGGATTGTTGAGATGCTAC

Db 282 TGTGCCCCTGAGACAGGAGCTCCAGGATTGTTGAGATGACAC

Qy 121 TGCACAGCCCTGCCCTCGCAGTACAAGAACGCTGGGCCACACAAATGCGACAT

Db 342 TGCATAGTGTGCCCCTCCCGAAGATAAGCATGAGCTTGTGAGATGACAC

Qy 181 TGCATCACCTGTGCTGTCATCAATGGTGTCAAGGTCACTGACAGCTACCTCTAT

Db 375 TGCATACTGTGTGTCACAAATGGGTCAGAGGCCACTGCACAAATACCTCTAT

Qy 241 GCTGTCTG 248

Db 435 GCTATCTG 442

RESULT 7

BB554624

LOCUS BB554624

DEFINITION 442 bp mRNA linear EST 15-AUG-2000

ACCESSION BB554624

VERSION 1

KEYWORDS EST

SOURCE house mouse.

ORGANISM Mus musculus

VERBOSITY 1

EST

REFERENCE 1 (bases 1 to 680)

AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, T., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

COMMENT Unpublished (2001)

JOURNAL Contact: Yoshihiko Hayashizaki¹

Sciences Center(GSC), Yokohama Institute

BASE COUNT

123 a

104 c

114 g

101 t

ORIGIN

1

Query Match

24.5%

Score 169.6;

DB 10;

Length 442;

Best Local Similarity

85.5%

Pred. NO. 2.4e-37;

Matches 212;

Conservative

0;

Mismatches 34;

Indels 2;

Gaps 2;

Qy 1 ATGGATTGCCAAGAAATGAGTACTGGGACCAATGGGAGCGTGTGACTGCCAACGG

Db 256 TGTGCCCCTGAGAGTGTACCGAGGCTCTCGCAGGATTGTTGAGAGGTGAGATGACAC

Qy 121 TGCACAGCCCTGCCCTCGCAGTACAAGAACGCTGGGCCACACAAATGCGACAT

Db 316 TGTGCTCTGGACAGGAGCTATCCAGGATTGTTGAGATGCTAC

Qy 181 TGCATCACCTGTGCTGTCATCAATGGTGTCAAGGTCACTGACAGCTACCTCTAT

Db 340 TGCATACTGTGTGTCACAAATGGGTCAGAGGCCACTGCACAAATACCTCTAT

Qy 241 GCTGTCTG 248

Db 435 GCTATCTG 442

RESULT 8

BB663265

LOCUS BB663265

DEFINITION 680 bp mRNA linear EST 26-OCT-2001

ACCESSION BB663265

VERSION 1

KEYWORDS EST

SOURCE house mouse.

ORGANISM Mus musculus

VERBOSITY 1

EST

REFERENCE 1 (bases 1 to 680)

AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, T., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

COMMENT Unpublished (2001)

JOURNAL Contact: Yoshihiko Hayashizaki¹

Sciences Center(GSC), Yokohama Institute

URL:<http://genome.gsc.riken.go.jp/>
 Carninci, P., Shihata, Y., Hayashi, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

Email: cgabps-r@mail.nih.gov

This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

MG:105280

Seq primer: -40RP from Gibco

High quality sequence stop: 425.

Location/Qualifiers

1. .442

/organism="Mus musculus"

/strain="FVB/N-3"

/db_xref="taxon:0090"

/clone="IMAGE:3153524"

/clone_lb="NCI_CGAP_Mam2"

/tissue_type="tumor, biopsy sample"

/dev_stage="5 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

QY	124	ACAGGCCCTCCGCGAGGTACAAAAGCACCTGGGGCACCACAAATGTCAGAGTGC	183
Db	373	GTCGCCCTCAGGCCGCCACGGTCAAGGAAGACTGGGTTCCAGAAGTGTAGCCATG	432
QY	184	ATCACCTGTGTCATCATGTCAGAGGTCACTGCACACTCTAATGTC	243
Db	433	GGGACTGTGCGCTGGTAACCGCTTCAGGGCCRACTGTCACACACAGGCTGAGCT	492
QY	244	GCTCTGGGAAGCTGTGTCAGGCTTCAAGGAAGACTGGGTTCCAGAAGTGTAGCCATG	303
Db	493	GTCGCGGGGACTGCGTCAGGATNTACGGAGAACCAACTGGTTGGTTCAAGAC	552
QY	304	CAAGAGTGCATCCCGTGCACGAGCACGAGCACCCACACTCTGAGGTCATGGCTGAGAC	363
Db	553	ATGGAGCTGTGCTCGAGACCCACCTCTCCCTACGAAACGACACTGTTACAGCAAG	612
QY	364	T ⁿ GAGCTTAGTGGAGGAGATGCCACAGTGCCCCCTAGGAGGAGCACACTGGTGC	422
Db	613	GTGAACCTTGGAAGATCTCTCACCGNGTCAGGCCCTCGGGACACGGCGTGGCTGC	671
RESULT	9		
LOCUS	BB650696		
DEFINITION	BB650696	616 bp	mRNA
ORGANISM	Mus musculus	linear	EST
REFERENCE	BB650696	enriched, 0 day neonate cerebellum Mus	26-oct-2001
AUTHORS	(bases 1 to 616)		
ACCESSION	BB650696		
VERSION	BB650696.1		
TITLE	EST.		
JOURNAL	house mouse.		
COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
CONTACT	Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute		
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH (RIKEN)	The Institute of Physical and Chemical Research (RIKEN)		
TEL:	1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
FAX:	81-45-503-9222		
Email:	genome-res@gsc.riken.go.jp,		
URL:	http://genome.gsc.riken.go.jp/		
Carrinci,P., Shibata,Y., Hayashizaki,Y., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okada,Y., Muramatsu,M. and Hayashizaki,Y.	Normalization and subtraction of cap trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. <i>Genome Res.</i> 10 (10), 1617-1630 (2000)		
Watabe,K., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunaga,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.	Computer-based methods for the mouse full-length cDNA encyclopedias: real-time sequence clustering for construction of a nonredundant cDNA library. <i>Genome Res.</i> 11 (2), 281-289 (2001)		
Kondo,S., Shinagawa,A., Saito,T., Kiosawa,H., Yamamoto,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. <i>Genome Res.</i> 10 (11), 1757-1771 (2000)		

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome*. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES e mouse tissues.
SOURCE Location/Qualifiers
I.: .616 " " "

Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'-GAGAGAGAGAGATCACAGCTTGTGTTTTTNTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full length by cap trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 479.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGATCTCCAGTTAATTAATTCGCCCGCCCC 3']. cDNA was cleaved with XbaI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC 1.

	Qy	4	GATGCCAACAAATGAGTACTGGGACCATGGGAGCGGTGTCACCTGCAACGGTT	63
BEST LOCAL SIMILARITY		19.5%	Score: 135; De-B: 9;	Length: 616;
Matches	219;	Conservative	60.9%; Pred.	No. 1-8e-27;
Mismatches	0;			Indels 0; gaps 0;
Db	168	GATTGCAGGAGCAGCAAGTCAAGGATCGAFCGTGGAACATGTGTCCTCTGCAACAGTG	C	227
Qy	64	GGTCCTGAGAAGGGAGGTATCAAGGATGTGTTATGGAAGGGTGGAGATGCCACTG	C	123
Db	228	GGACCTGGCATGGAGTGTCAAGGAATGTTGGCTATGGGAGGGTGCACAGTGT	C	287
Qy	124	ACAGGCTGCCTCTGGCACTACAAAGACGTGGCCACCACAAATGCAAGTCAG	C	183
Db	288	GTGCCCTGCAAGCCGGACCCGTTCAAGGAAGACTGGTTCCAGAGTGTAA	GT	347
Qy	184	ATCACCTGTCCTGTCATCAACGTGTCAGAGGTCAACGCCACGCTACTCTTA	ATG	243
Db	348	GCGGACTGTGCGCTGGTAACCGCTTTCAGAGGCCACTGTCTCACACCCAGTGT	GT	407
Qy	244	GTCTGTGGGACTGTGTTGCCAGGTCTACCGAAAGCACGCCATTGGAGGCC	TG	303
Db	408	GTCTGTGGGACTGTGTTGCCAGGTCTACCGAAAGCACGCCATTGGAGGCC	TG	467
Qy	304	CAAGACTGCACTCCGGTCAGCAAGCAGCACCCACCTCTGGTTCAATGTC	CG	363
Db	468	ATGGAGTGTGNGCCCTGGGAGACCCACCTCTCCCTACCGAACACAGTGT	ACCGAG	527

RESULT 1

LOCUS BE306459 395 bp mRNA linear EST 26-OCT-2000
DEFINITION 60110349f1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3495566 5',
ACCESSION mRNA sequence.
VERSION BE306459
KEYWORDS BE306459.1 GI:9159707
EST.
SOURCE house mouse.

	MUS	MUSCULUS	ORGANISM
FEATURES	Mammalia;	Metazoa;	Chordata;
source	Eutheria;	Rodentia;	Craniate;
	Sciurognathi;	Muridae;	Guteleostomi;
	1	(bases 1 to 395)	Mus;
REFERENCE	NIH-MGC	http://mgc.nci.nih.gov/	
AUTHORS	National Institutes of Health,	Mammalian Gene Collection (MGC)	
TITLE	Unpublished	(1999)	
JOURNAL	Contact:	Robert Strausberg, Ph.D.	
COMMENT	Email:	cabps-r@mail.nih.gov	
	Tissue Procurement:	Gilbert Smith, Ph.D.	
	CDNA Library Preparation:	Life Technologies, Inc.	
	CDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LLNL)	
	DNA Sequencing by:	Incyte Genomics, Inc.	
	Clone Distribution:	MGC clone distribution information can be	
	found through the I.M.A.G.E. Consortium/LLNL at:		
		http://image.llnl.gov	
	Plate:	L1AM8546	row: f
		column: 15	
	High quality sequence stop:	395.	
	Location/Qualifier		
	I.	395	
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	/strain="CZECH II (feral)"		
	/db_xref="TAXON:10090"		
	/clone="IMAGE:3495566"		
	/clone_1_id="NCI_CGAP_Lu29"		
	/tissue_type="Spontaneous tumor, metastatic to mammary.		
	stem cell origin."		
	/lab_host="DHIB"		
	/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.		
	Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"		
BASE COUNT	88	a	
ORIGIN	101	c	
	120	g	
	86	t	

ORGANISM	Oryzias latipes
BELONIIFORMES	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleosteii; Acanthomorpha; Acanthopterygii; Percomorpha; Athetinomorpha; Beloniiformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE	Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H.
AUTHORS	Medaka EST Project in Takeda's lab
TITLE	Unpublished (2001)
JOURNAL	Contact: Tadasu Shin-i
COMMENT	Center For Generic Resource Information National Institute of Genetics 111 Yata, Mishima, Shizuoka 411-8540, Japan tel: 81-555-81-6856 Fax: 81-555-81-6855 Email: tshini@genes.nig.ac.jp
FEATURES	Location/Qualifiers
SOURCE	1. . 589
Query Match	/organism="Oryzias latipes" 'strain="Hd-rR"' 'db_xref="Taxon:8090'" 'clone="MF01SSA062F09'" 'clone.lib="MF01SSA_CDNA'" 'sex="mixture of female and male'" 'tissue_type="whole embryo"' 'dev_stage="segmentation stage 20 - 25"'
BASE COUNT	122 a 165 c 183 g 118 t 1 others
ORIGIN	
Query Match	17.7%; Score 122.4; DB 10; Length 589;
Best Local Similarity	58.1%; Pred: No. 6.7e-24;
Matches	216; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
QY	4 GATGCCAAAGAAATGNTACTGGACCAATGGGACGGTGTACCTGCCAACGGTGT 63
Db	200 GATGCCAAAGAAATGNTACTGGACCAATGGGACGGTGTACCTGCCAACGGTGT 259
QY	64 GATGCCAAAGAAATGNTACTGGACCAATGGGACGGTGTACCTGCCAACGGTGT 123
Db	260 GATGCCAAAGAAATGNTACTGGACCAATGGGACGGTGTACCTGCCAACGGTGT 319
QY	124 ACAGCCTCGCCCTCTCGCAGGATCAAAGAACGACCTGGGCCACACAATGTCAGASTGC 183
Db	320 GTGCCCTCGCGAGCAGTCGTCATACTGGTGTACAGAGGTCAACTGACAGCTACCTTAATGCT 243
QY	184 ATCACCTGTCGTCATACTGGTGTACAGAGGTCAACTGACAGCTACCTTAATGCT 243
Db	380 CTGACTGTCCTCATCACCGCTTCAGGAGCAAGGCACCTGTCACCGCAAGGC 439
QY	244 GTCTGTGGGAGCTGTTGCCAGGTCTACCGAAAGACGGATTGGAGGCTGAGGAC 303
Db	440 GTCTGTGGGAGCTGTTGCCAGGTCTACCGAAAGACGGATTGGAGGCTGAGGAC 499
QY	304 CAAAGACTCATCCGTCGACAGGAGCACCCACCTCTGAGATTCAGTGGATCCAGGAC 363
Db	500 ATGGAGGTCATACCTGTGGGACACCTCCTATGAGCCAACTGTAGTGGGGT 559
QY	364 TTAGCTGTAGT 375
Db	560 GTCACACCTGGT 571
RESULT	12
BF162288	BF162288
LOCUS	BF162288
DEFINITION	60177086F1 NCL-CGAP_Lu29 Mus musculus cDNA clone IMAGE:3990285 5', mRNA sequence.
ACCESSION	BF162288
VERSION	BF162288.1 GI:11042496
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens
RESULT	13
BT919139	BT919139
LOCUS	BT919139
DEFINITION	60318457F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5248745 5', mRNA sequence.
ACCESSION	BT919139
VERSION	BT919139.1 GI:16200214
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
RESULT	14
BT919139	BT919139
LOCUS	BT919139
DEFINITION	932 bp mRNA linear EST 16-OCT-2001
ACCESSION	BT919139
VERSION	BT919139.1 GI:16200214
KEYWORDS	EST.
SOURCE	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 932)	NIH-MGC	http://mgc.ncbi.nlm.nih.gov/		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
Unpublished (1999)				Mus musculus;
Contact: Robert Straussberg, Ph.D.				Bukarrotua; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
Email: cgsbs-r@mail.nih.gov				Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoaka,T., Hirozane,T., Imotani,K., Ishii Y., Ito,M., Kawai,J., Koijima,Y., Konno,H., Kouda,M., Matsunaga,T., Nakamura,M., Nishii,K., Nomura,R., Nomura,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sobagye,Y., Suzuki,H., Tagawa A., Takahashi,F., Takaku,Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watanuki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
Tissue Procurement: Life Technologies, Inc.				found through the T.M.A.G.E. Consortium/LNLL at:
cDNA Library Preparation: Life Technologies, Inc.				http://image.lnll.gov
DNA Sequencing by: The T.M.A.G.E. Consortium (LNLL)				Plate: LLM11627 row: o column: 18
Clone distribution: Incyte Genomics, Inc.				High quality sequence start: 28
Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LNLL at:				High quality sequence stop: 723.
High quality sequence stop: 723.				Location/Qualifiers
1. .932				1. organism="Homo sapiens"
Best Local Similarity 61.0%; Score 100.6; DB 10; Length 932; Matches 197; Conservative 0; Mismatches 124; Indels 2; Gaps 2;				/db_xref="taxon:9606"
QY 19 GAGTACMRGGCCAARGGGGACGGGTCACCTGCCAACCGTGTTGCTCTGGACAGAG 78				/clone_1ib="NIH-MGC_121"
Db 448 GATTCAGGGATCCTGGCTGAACTGTGTTCTGCACACCTGAGCTGGAGATGCTCCACTGCACAGCTGCCCTCCT 507				/lab_host=DH10B"
Qy 79 CTATCCAGGATTGGTGTATGGAGGGTGGAGATGCTCCACTGCACAGCTGCCCTCCT 138				/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, male age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH-MGC Library "
Db 508 TTTGCTTAAAGATGAGTGGCTTGGCTATGGGGAGGAGTCAAGTGTGTGAGAGGGCTG 567				BASE COUNT 242 a 222 c 234 g 234 t ORIGIN
QY 139 CGCGAGGTACAAAGAGCTGGGGCACCAATGTCAG AGTTGGCATCATCTGGCTGT 197				FEATURES SOURCE
Db 568 CACAGTTCAAGGGAGCTGGGCTTCCAGAATGCAGCCCTGCTGACTGCCCAGT 627				1. .519
Qy 198 CATCAATCGTGTTCAGAAGTC-ACTGCAAGCTTCT-TAATGGTGTCTGGGACT 256				organism="Mus musculus"
Db 628 GGTGAACCGCTTCAAGGCAACATGTGTCAAGCCTGGGAGACT 687				/strain="C57BL/6J"
QY 257 GTTGGCCAGGGTCTACCGAAGACGACGCTTGGAGCTTGGAGGACTGATCC 316				/db_xref="taxon:10090"
Db 688 GCTTGGCCAGGAACTCATAGGAAGACGAACTGTGGCTTCAAGACATGAGTGTG 747				/clone="G370041G09"
Qy 317 CGTGACAGAGCAGCCCCACC 339				/clone_1ib="Riken full-length enriched, B16 F10Y cells"
Db 748 CTTGTACAGAAAGACCCCTCCATC 770				/cell_type="B16 F10Y cells"
RESULT 14				BASE COUNT 112 a 1138 c 167 g 102 t ORIGIN
BB857078				FEATURES SOURCE
BB857073				EST. house mouse.
DEFINITION				519 bp mRNA linear EST 26-NOV-2001
ACCESSION				cDNA clone G370041G09 5', mRNA sequence.
VERSION				BB857078.1 GI:17098532

RESULT 15
 BE757704
 LOCUS BE757704
 DEFINITION 212225 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BE757704.1
 VERSION GI:10171696
 KEYWORDS EST.
 SOURCE
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE
 AUTHORS Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
 Casas, E., Wray, J.E., White, J., Cho, J., Fahrerkrug, S.C., Bennett,
 G.L., Henton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G.,
 Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
 Keele, J.W.
 TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
 JOURNAL Genome Res. 11 (4), 626-630 (2001)
 MEDLINE 21180013
 COMMENT Contact: Smith, TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt_trimmed with phred
 v0.960904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.
 PCR PRIMERS
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCACACTCACACAG
 PLATE: 65
 ROW: C
 COLUMN: 2
 SEQ PRIMER: ATTTAGGAGACATATAG
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 /lab_host="DH10B"
 /note="vector: pCMV SPOR6; Site_1: XbaI; Site_2: XhoI;
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 semitendinosus muscle, longissimus muscle, pancreas,
 adrenal, and endometrium."
 BASE COUNT
 ORIGIN
 122 a 171 g 124 t
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 Best Local Similarity 60.8%; Pred. No. 4e-15;
 Matches 149; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

OY	4	GATTGCCAAGAAATGAGTACTGGGACCACTGGGGAGGTGTCACCTGCCAACGGTGT	63	Db	409	GTGAGTGCGGCCACAGGTCAGAGGACTGGGCTCTAGAAGTGCAAGCCGTC	468
Db	289	GAATGTGAGCACGCCAGGAATTGGGGACAGTCAGGAGCTGTCAGGAGCTGTTCTGAG	348	OY	184	ATCACCTGCTGTCATCATCGTGTCTGAAGTCACACTGCACAGC"ACCTTAATGCT	243
OY	64	GCTCCCTGACAGAGCTATCCAGGATTGTCGTTATGGAGGGTGAGATCCCTACTGC	123	Db	469	CTGGACTGCCCTGCTGAGCCGCTTCAGAAGGCCACTGGGACCC	528
Db	349	GGCCCAAGCATGGATGTCAGGAGATGTCAGGAGCTGTCAGGAGCTGTCAGCTG	408	OY	244	GTCCTG 248	
OY	124	ACAGCCCTGCCCTGCCAGGTACAAAGCACGCTGGGCCACACAATGTCAGAGSTGC	183	Db	529	GTCIG 533	

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